APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS
	435	69.1

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1/25

6436670

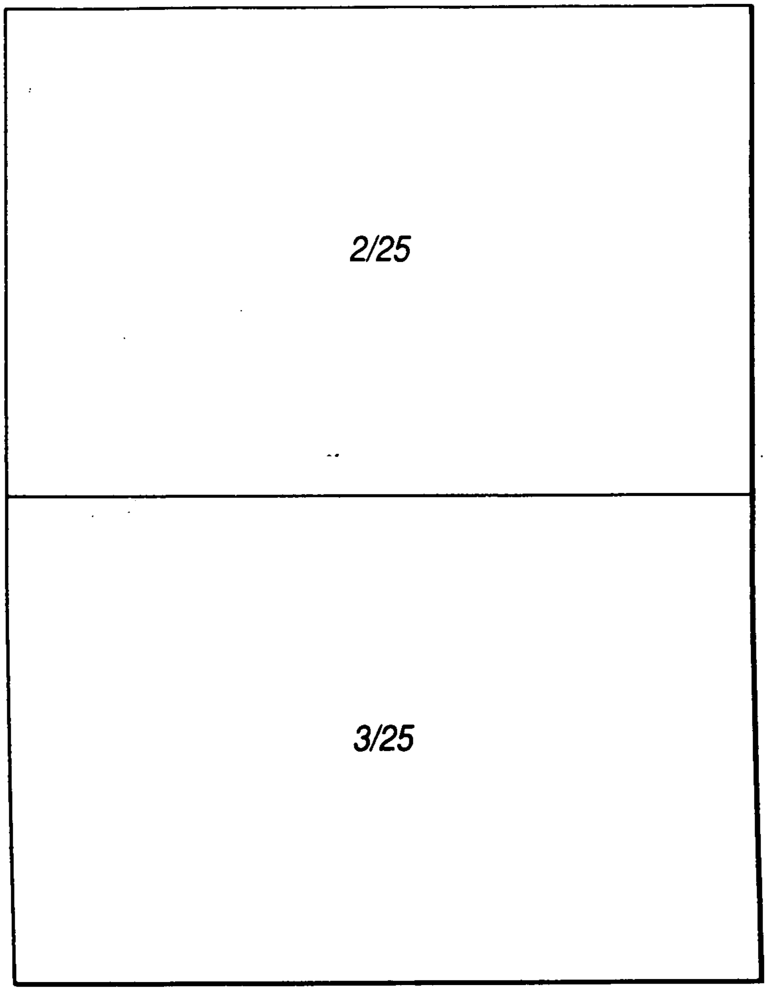

Fig.1A

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS 435 | SUBCLASS 69.1

```
                                   50                                 60
 K   I   V   L   K   K   W   Y   T   I   F   K   D   H   V   S   L   G   D   Y
AAGATCGTTCTTAAAAAGTGGTACACGATTTTTAAGGACCATGTATCTCTGGGAGATTAT
TTCTAGCAAGAATTTTTCACCATGTGCTAAAAATTCCTGGTACATAGAGACCCTCTAATA

                                   70
 E   I   H   D   G   M   N   L   E   L   Y   Y   Q   STOP
GAAATCCACGATGGGATGAACCTGGAGCTTTATTACCAGTAGAGGGGAATTCCTCCACC
CTTTAGGTGCTACCCTACTTGGACCTCGAAATAATGGTCATCTCCCCTTAAGGAGGTGG

TTGCCCAACCTTGCTTTCCTCTCCCATGGCTCATTTAACACTGTTGTAGATGCTCATTTTT
AACGGGTTGGAACGAAAGGAGAGGGTACCGAGTAAATTGTGACAACATCTACGAGTAAAAA

AACAATTCACATGAATAAAAACTTTGATGCTGCAAAAAAAAA   3'
TTGTTAAGTGTACT   5'
```

Fig.1A (i)

50 60

K I V L K K W Y T I F K D H V S L G D Y

AAGATCGTTCTTAAAAAGTGGTACACGATTTTTAAGGACCATGTATCTCTGGGAGATTAT

TTCTAGCAAGAATTTTTCACCATGTGCTAAAAATTCCTGGTACATAGAGACCCTCTAATA

70

E I H D G M N L E L Y Y Q STOP

GAAATCCACGATGGGATGAACCTGGAGCTTTATTACCAGTAGAGGGGAATTCCTCCACC

CTTTAGGTGCTACCCTACTTGGACCTCGAAATAATGGTCATCTCCCCTTAAGGAGGTGG

TTGCCCAACCTTGCTTTCCTCTCCCATGGCTCATTTAACACTGTTGTAGATGCTCATTTTT

AACGGGTTGGAACGAAAGGAGAGGGTACCGAGTAAATTGTGACAACATCTACGAGTAAAAA

AACAATTCACATGAATAAAAACTTTGATGCTGCAAAAAAAAA 3'

TTGTTAAGTGTACT 5'

Fig.1A (ii)

```
ATG ATC GAG GTT GTT TGC AAC GAC CGT CTG GGG AAA AAG GTC CNC  45
Met Ile Glu Val Val Cys Asn Asp Arg Leu Gly Lys Lys Val Xaa
  1           5                  10                  15

GTT AAA TGC AAC ACG GAT GAT ACC ATC GGG GAC CTT AAG AAG CTG  90
Val Lys Cys Asn Thr Asp Asp Thr Ile Gly Asp Leu Lys Lys Leu
                 20                  25                  30

ATT GCA GCC TAA                                             102
Ile Ala Ala *
```

Fig.1B

09/331930

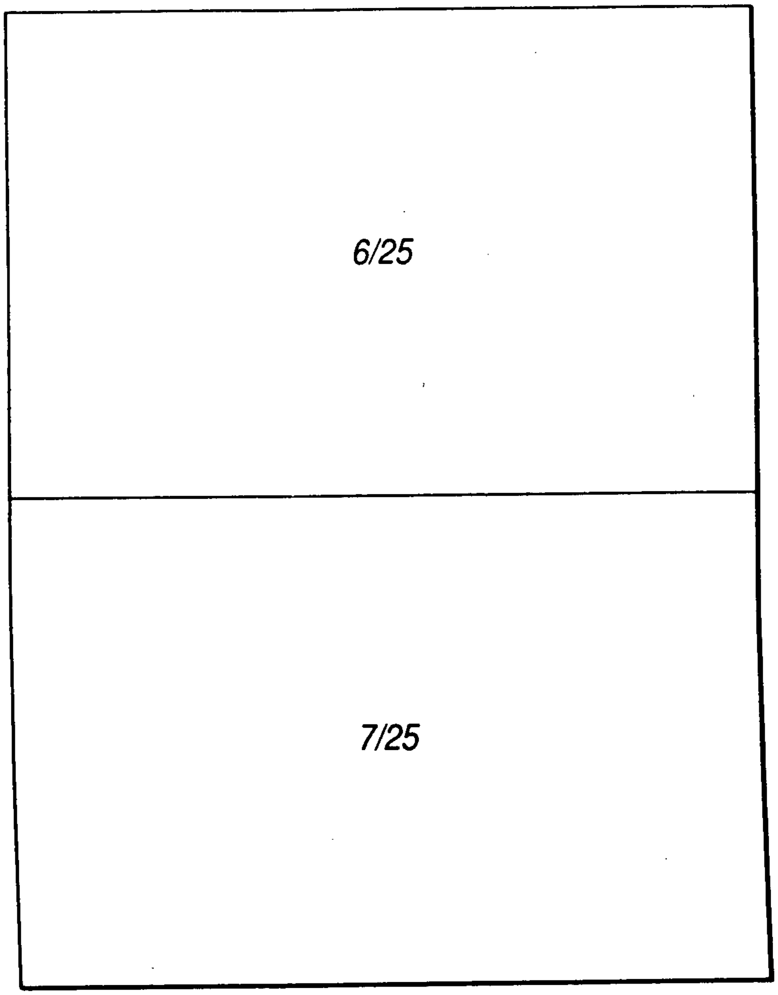

Fig.2A

AMINO ACID ALIGNMENTS

A.

```
                    10        20        30        40        50
                     *         *         *         *         *
Beacon      MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
Human       MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
Mouse       MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
C.elegans   MIEITVNDRLGKKVRIKCNPSDTIGDLKKLIAAQTGTRWEKIVLKKWYTI
F.hepatica         DRLGKKVRVKCNPTDKVGDLKKLIAAQTGTAPERIVLKKWYTI
Rice        MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
S.cerev     MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
```

Fig.2A (i)

	60 70
	* *
Beacon	FKDHVSLGDYEIHDGMNLELYYQ
Human	FKDHVSLGDYEIHDGMNLELYYQ
Mouse	FKDHVSLGDYEIHDGMNLELYYQ
C.elegans	YKDHITLMDYEIHEGFNFELYYQ
F.hepatica	YKDHVTLRDYEINDGMNLELYYQ
Rice	YKDHITLADYEIHDGMGLELYYN
S.cerev	LKDHICLEDYEVHDQTNLELYYL

Percentage	homologies
Human	73/73 = 100%
Mouse	73/73 = 100%
C.elegans	59/73 = 81%
F.hepatica	54/66 = 82%
Rice	58/73 = 79%
S.cerev	46/73 = 63%

Fig.2A (ii)

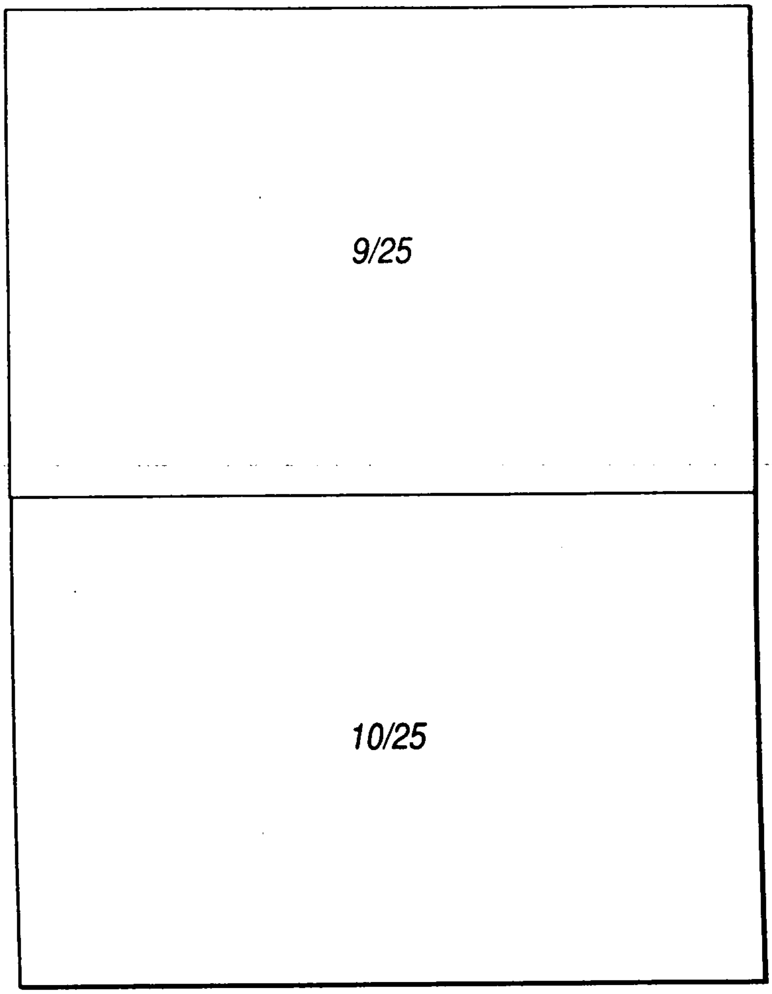

Fig.2B

APPROVED BY DRAFTSMAN
O.G. FIG.
CLASS 435
SUBCLASS 69.1

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B.

Human ubiquitin

```
                   10        20        30        40        50
                    *         *         *         *         *
Beacon      MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
             | |      || + ++    ||| ++|  |  + |   ++  |
Ugiquitin  MQIFVKT  LTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQ

                    60        70
                     *         *
Beacon     FKDHVSLGDYEIHDGMNLELYYQ
            +|  +| ||+|     | |
Ubiquitin  LEDGRTLSDYNIQKESTLHLVLRLRGG
```

Amino acid homology 18/73 = 25%

Positives (similar amino acids) 29/73 = 40%

Fig.2B (i)

Ubiquitin-like protein 8 (A. thaliana)

```
                    10        20        30        40        50
                     *         *         *         *         *
Beacon      MIEVVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNKIVLKKWYTI
                      || + ++  + ||| ++|+ |  + |   ++ +|  +
A. thaliana           GKTIILEVESSDTIANVKEKIQVKEGIKPDQQMLIFFGQQ

                    60        70
                     *         *
Beacon      FKDHVSLGDYEIHDGMNLELYYQ
             +| |+||||+||    | |
A. thaliana LEDGVTLGDYDIHKKSTLYL
```

Amino acid homology 19/60 = 32%

Positives (similar amino acids) 34/60 = 57%

Fig.2B (ii)

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS 435 | SUBCLASS 69.1

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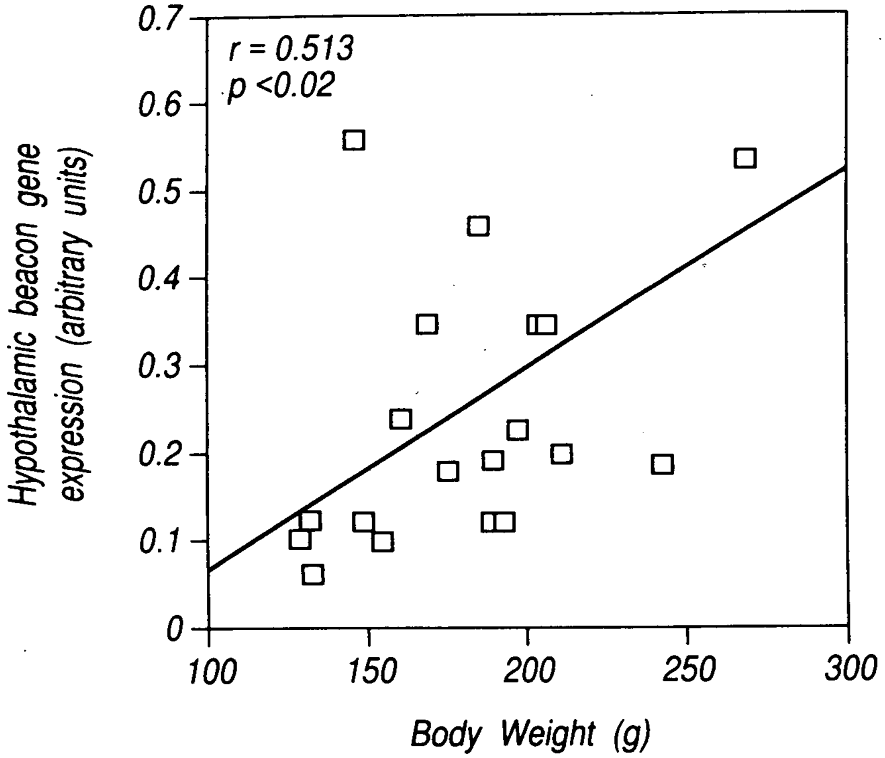

Fig.3A

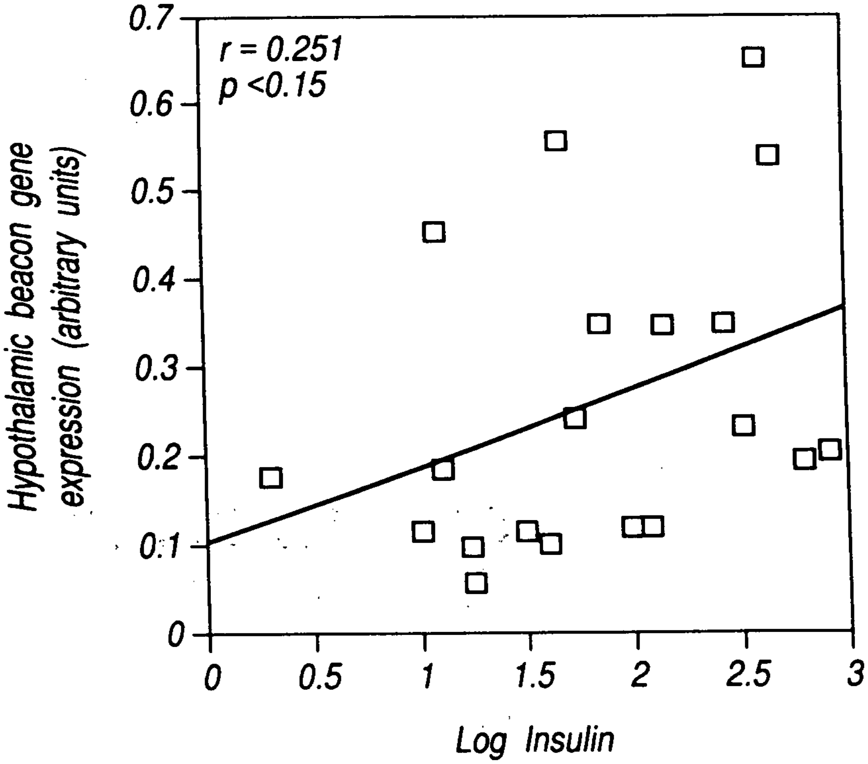

Fig.3B

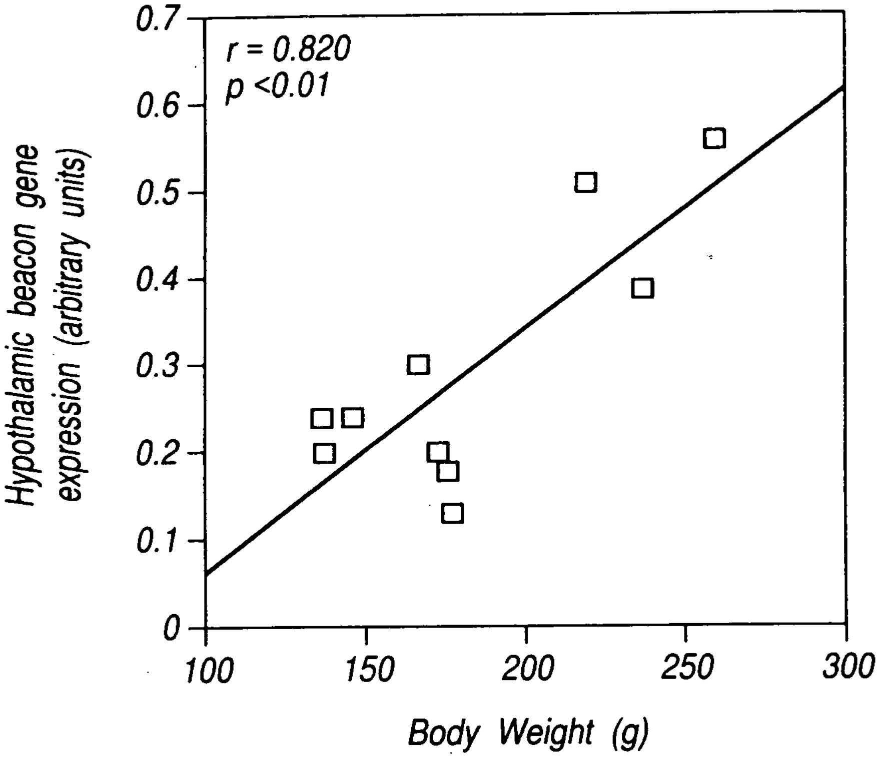
r = 0.820
p <0.01
Hypothalamic beacon gene expression (arbitrary units)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
100
150
200
250
300
Body Weight (g)

Fig.4A

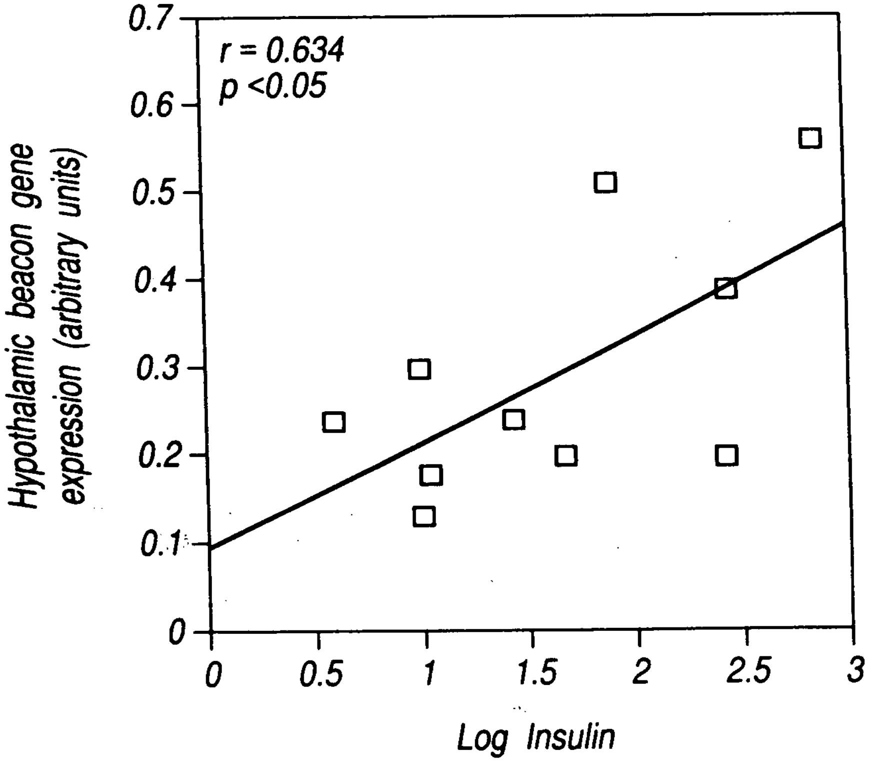
r = 0.634
p <0.05
Hypothalamic beacon gene expression (arbitrary units)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
0.5
1
1.5
2
2.5
3
Log Insulin

Fig.4B

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS 435 | SUBCLASS 69.1

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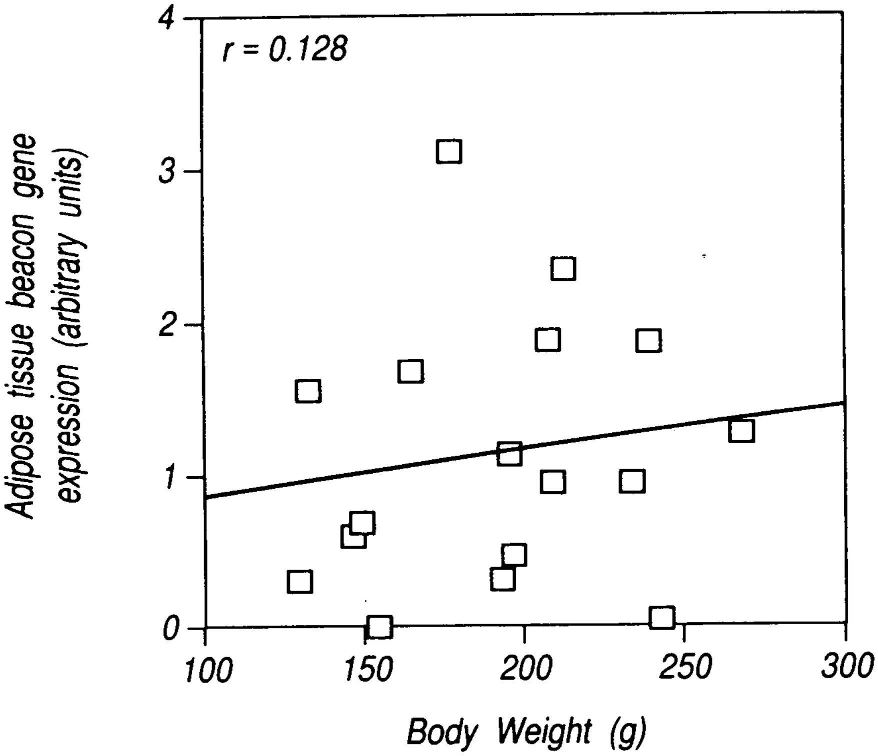

Fig.5A

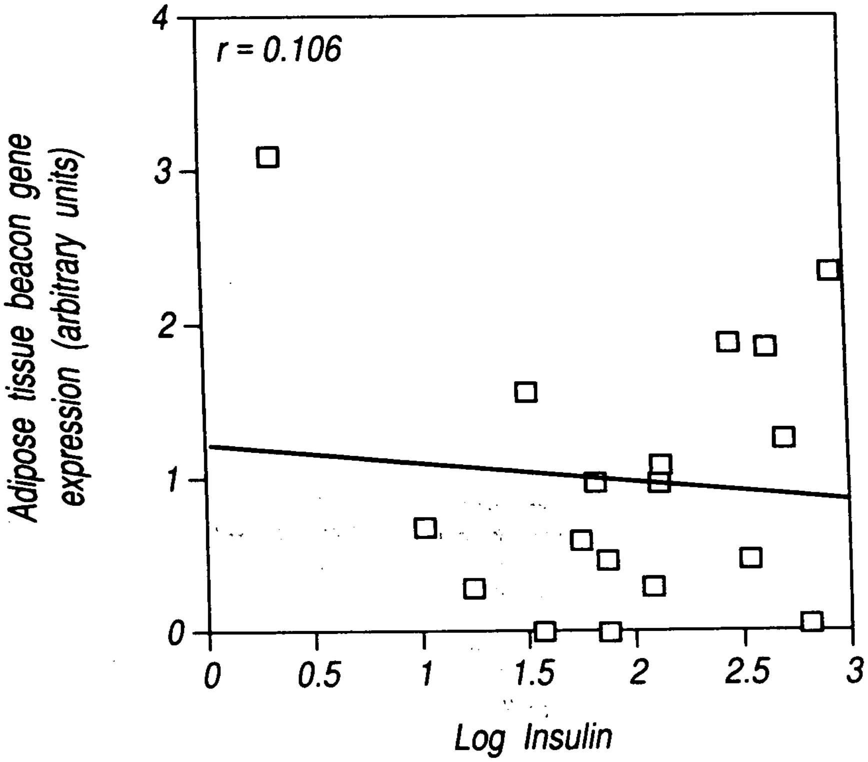

Fig.5B

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS
	435	69.1

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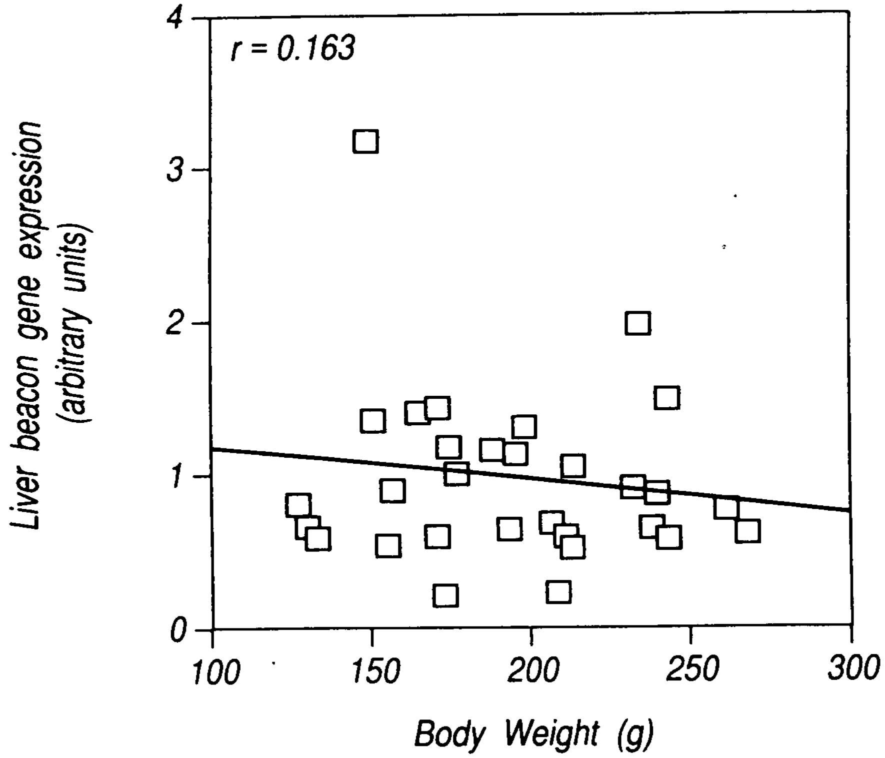


Fig.5C

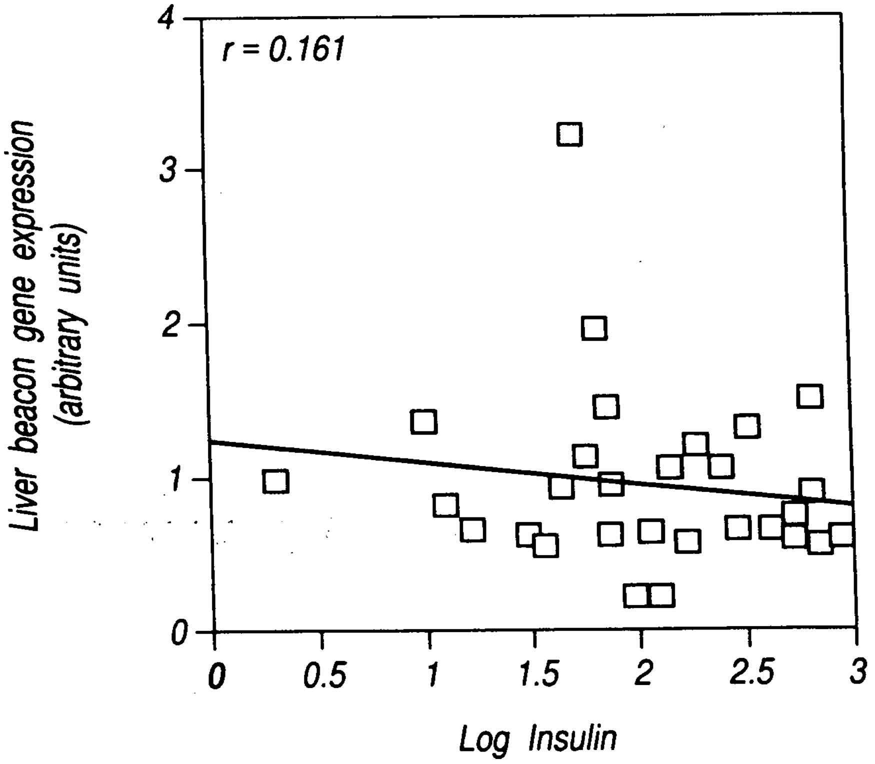


Fig.5D

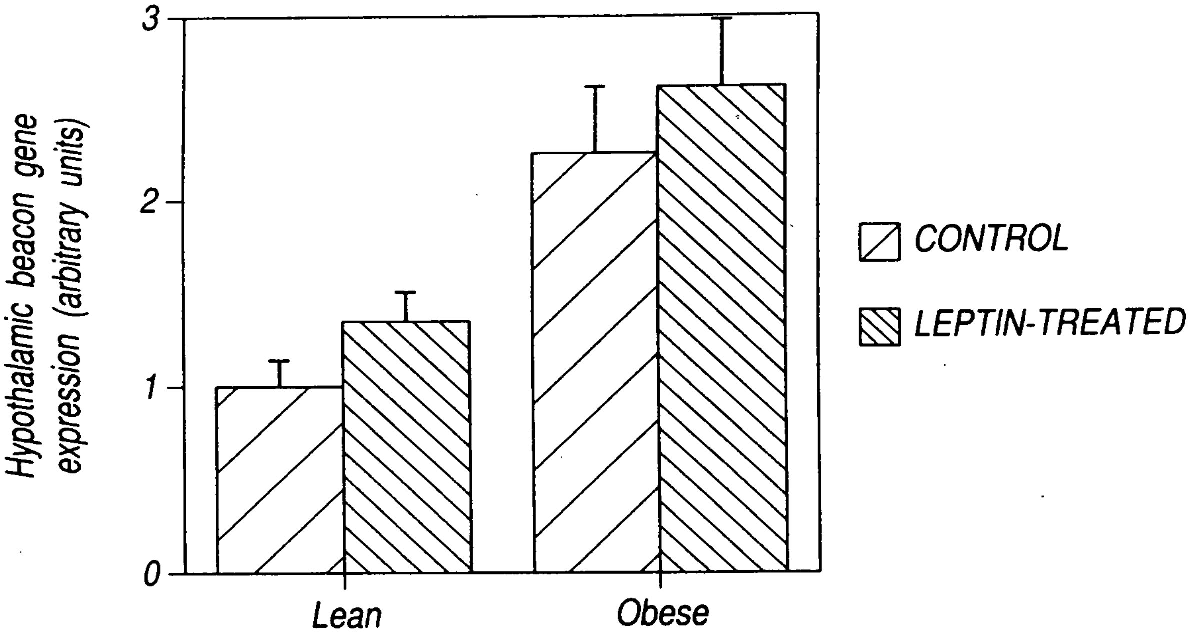

Hypothalamic beacon gene expression (arbitrary units)
0
1
2
3
Lean
Obese
CONTROL
LEPTIN-TREATED

Fig.6

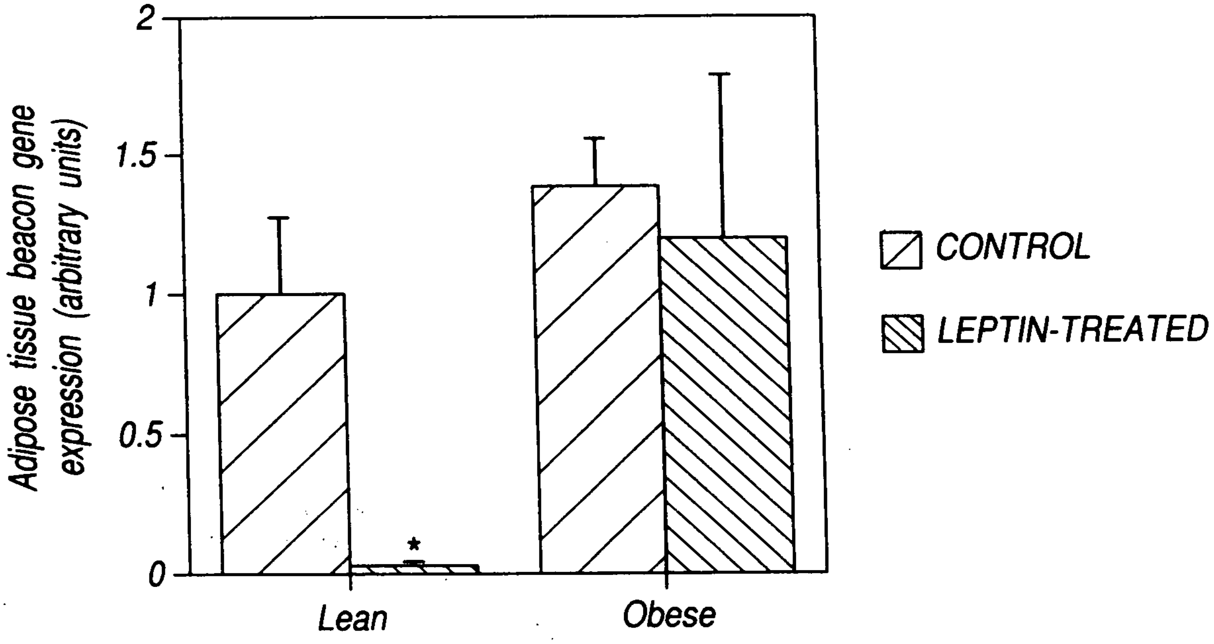

Adipose tissue beacon gene expression (arbitrary units)
0
0.5
1
1.5
2
*
Lean
Obese
CONTROL
LEPTIN-TREATED

Fig.7

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS 435 | SUBCLASS 69.1

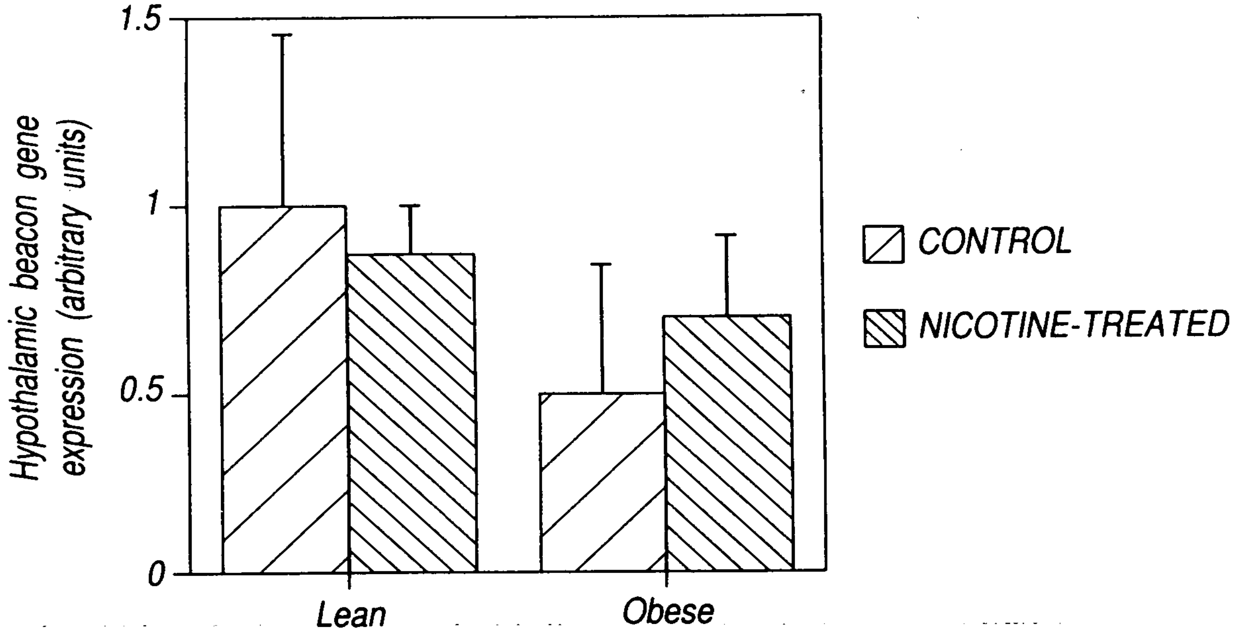


Fig.8A

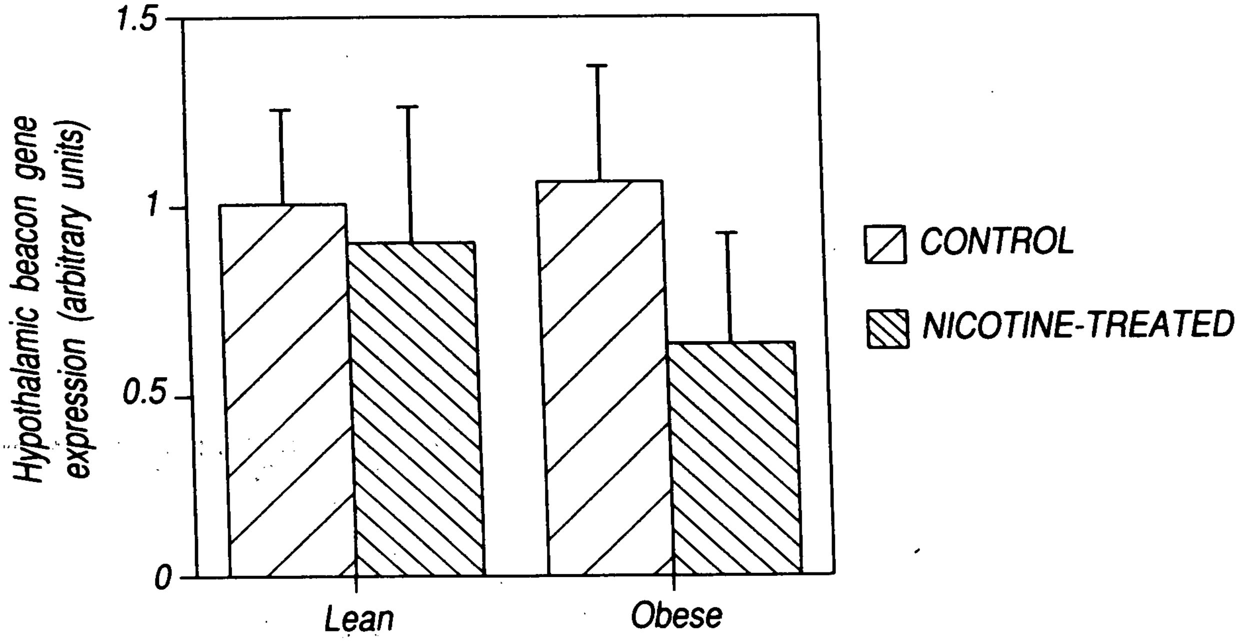


Fig.8B

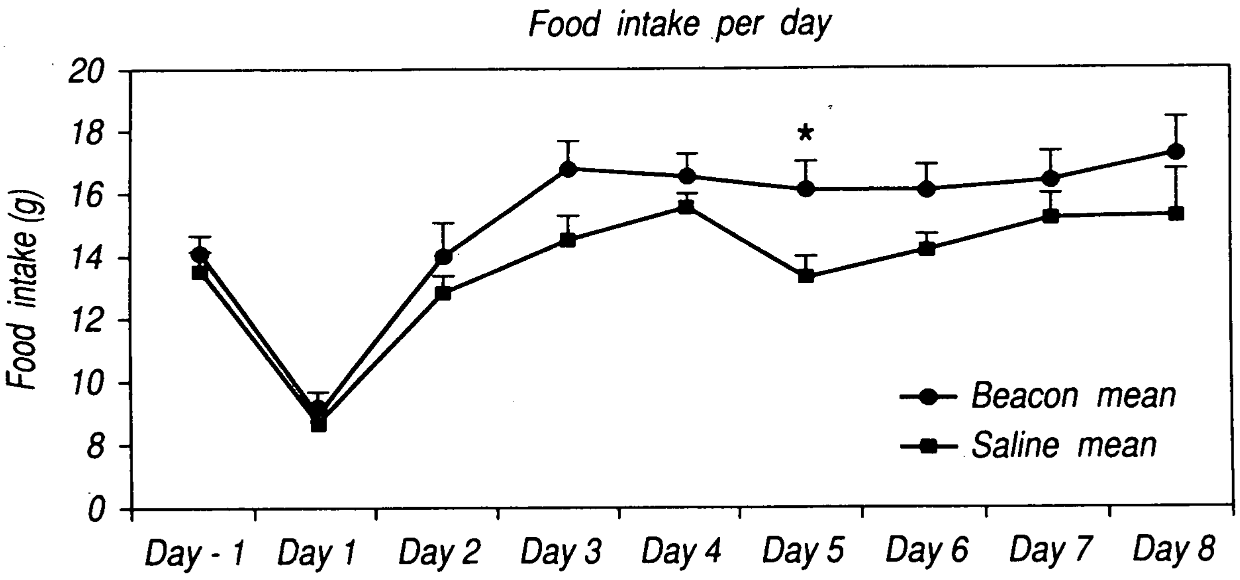
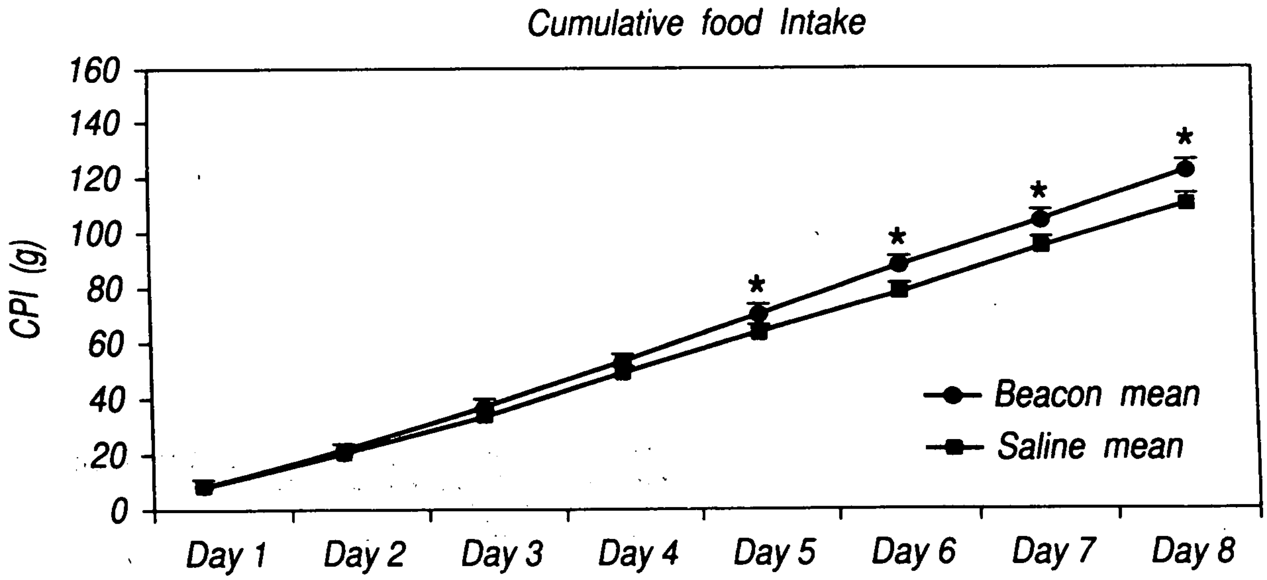


Fig.9A



* = significant, $p<0.05$

Fig.9B

09/331930

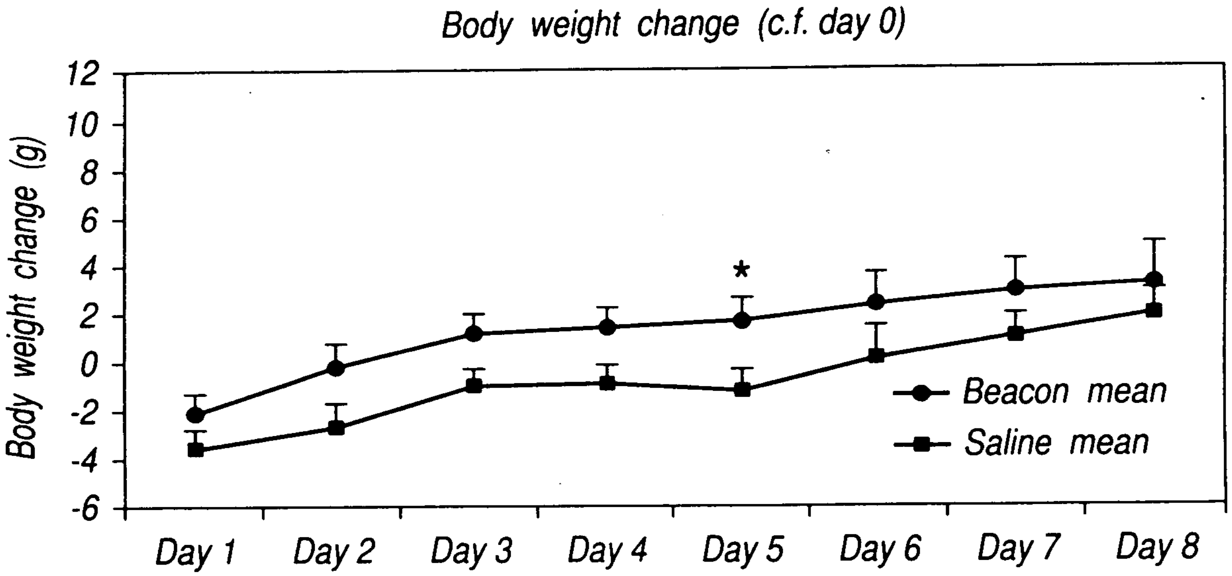


Fig.9C

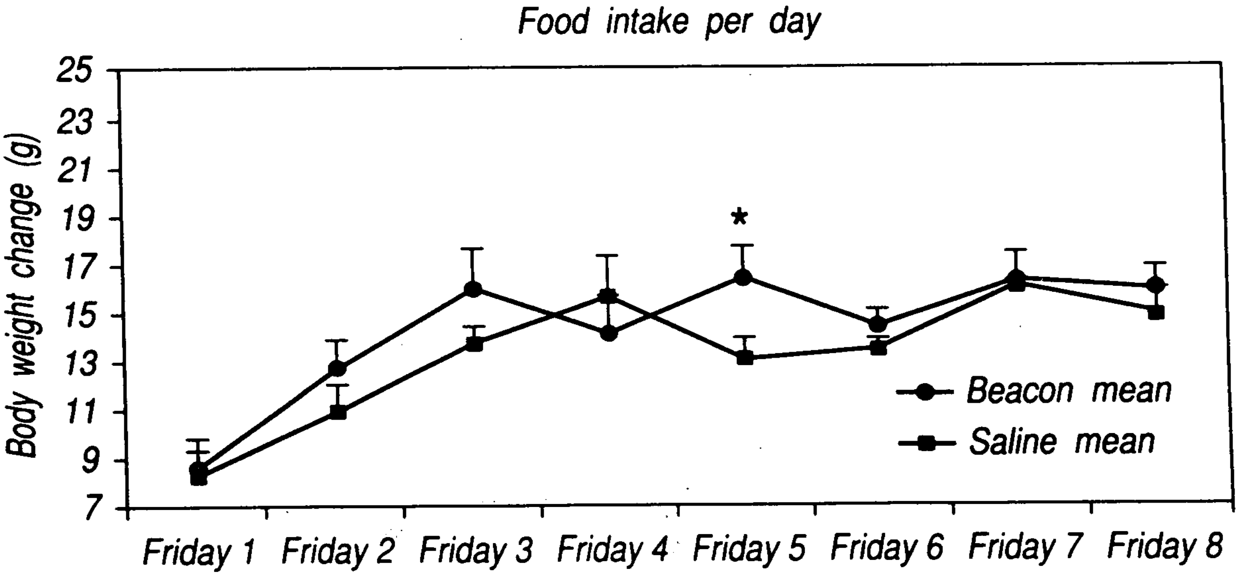


Fig.10A

* = significant, $p<0.05$

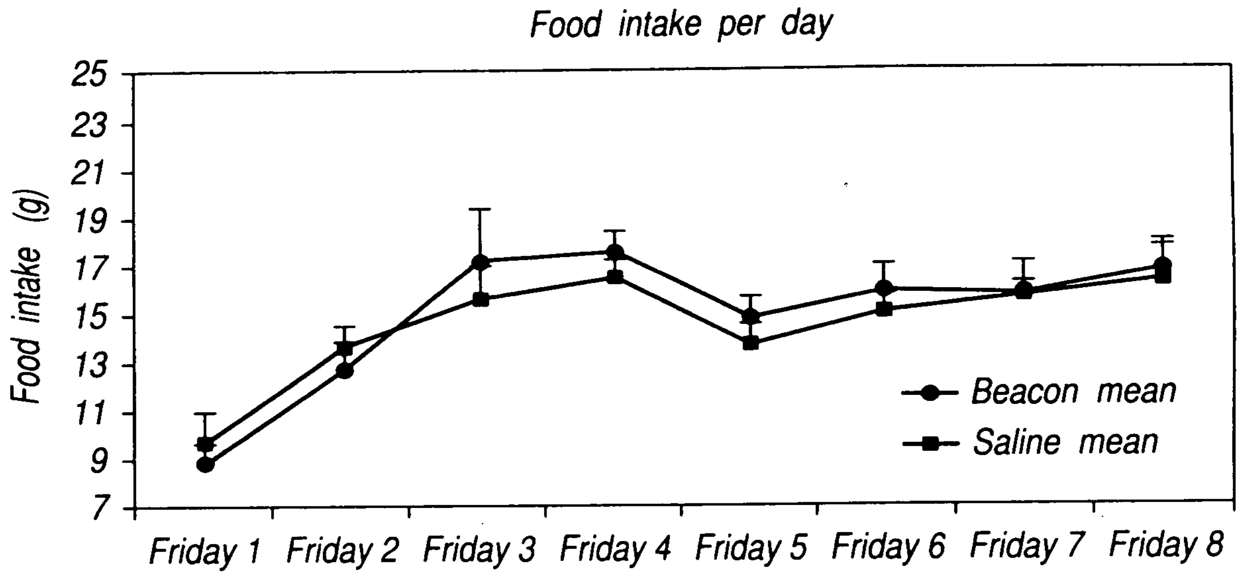


Fig.10B

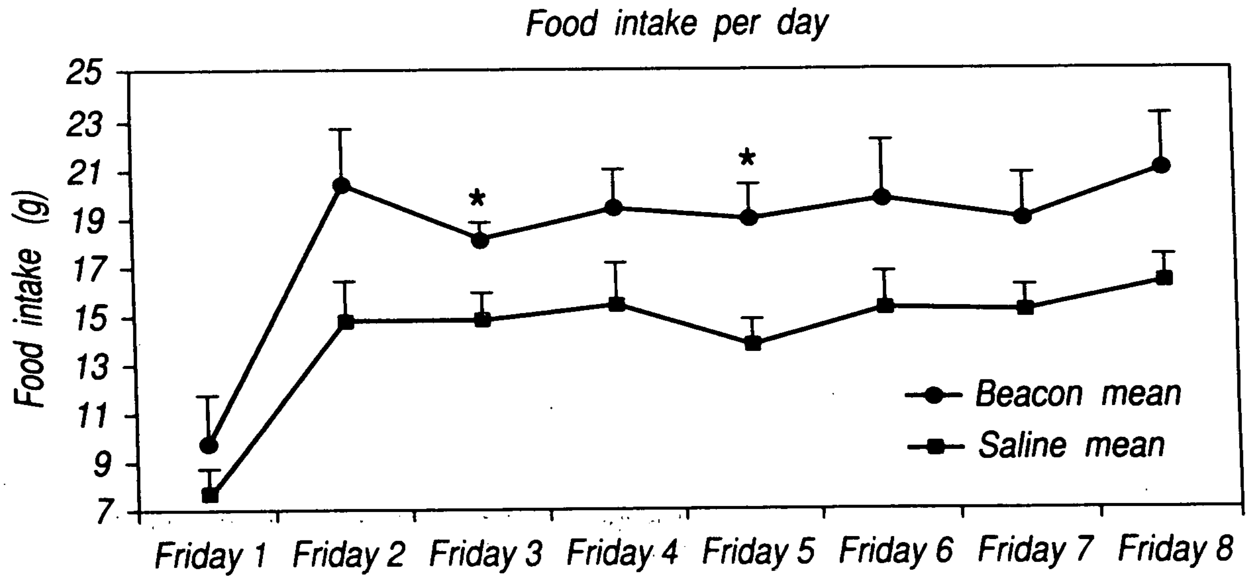


Fig.10C

* = significant, $p<0.05$

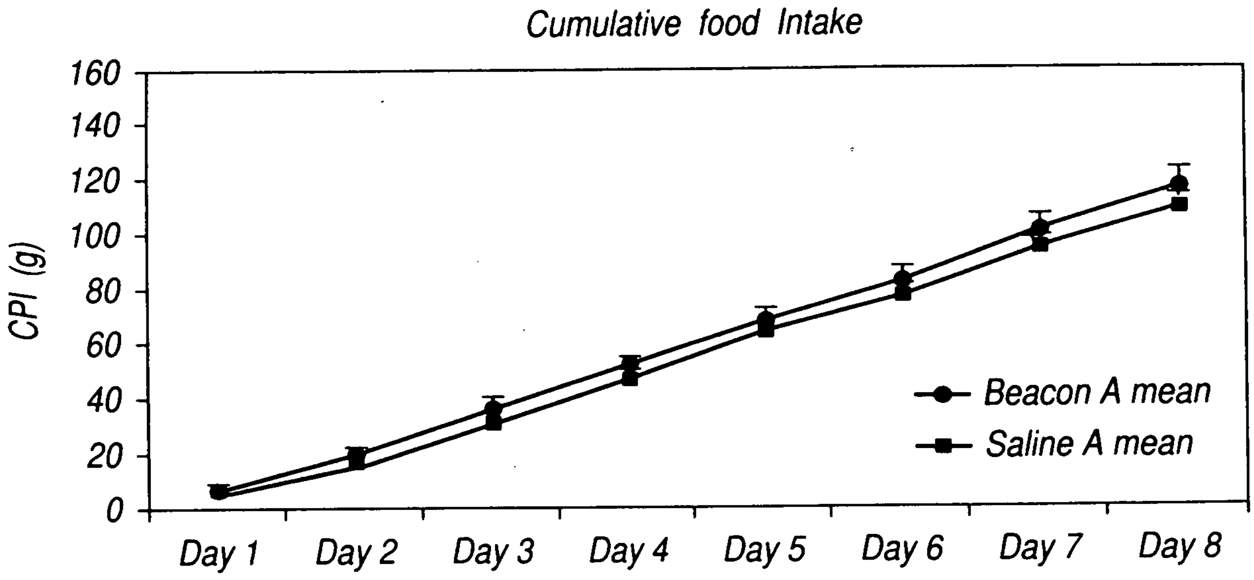
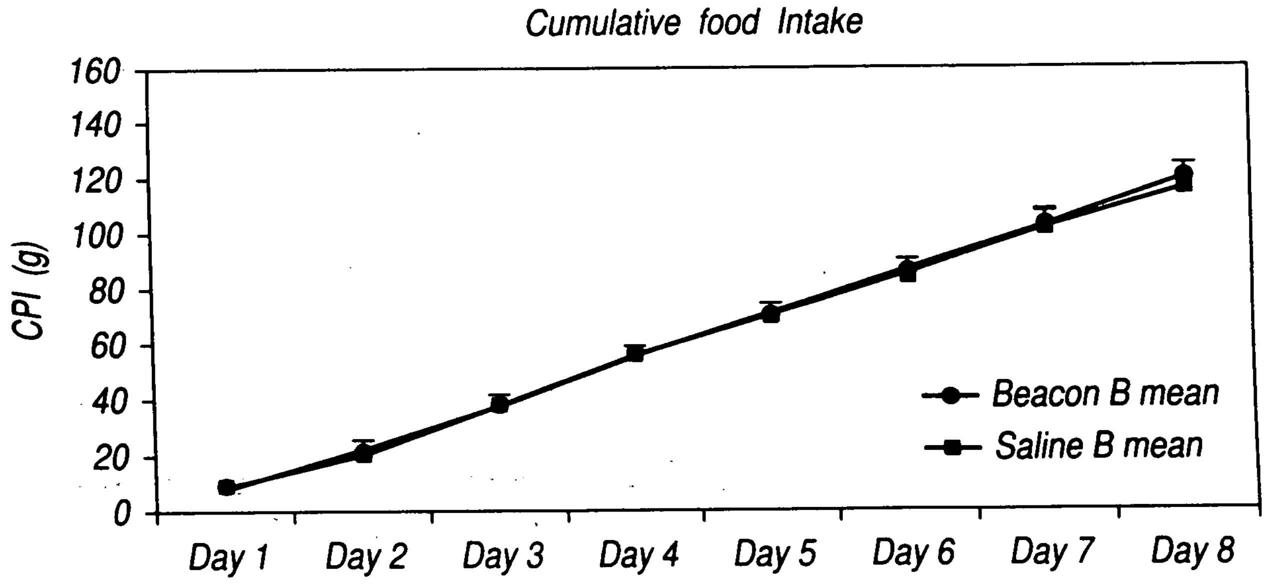


Fig.11A



* = significant, $p<0.05$

Fig.11B

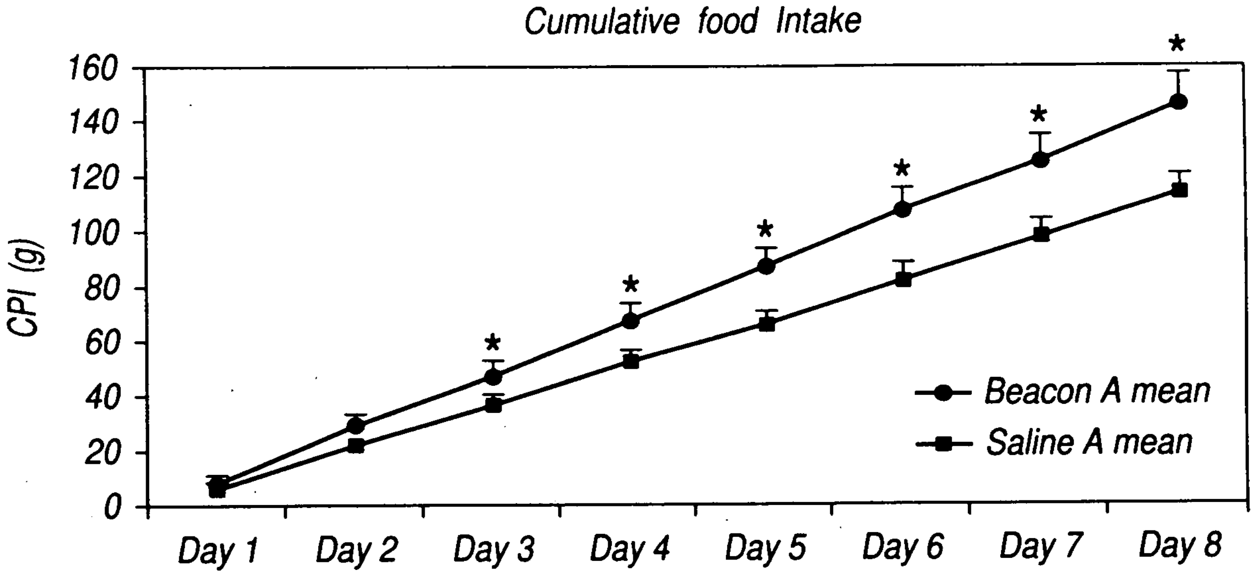

Cumulative food Intake
CPI (g)
160
140
120
100
80
60
40
20
0
Day 1
Day 2
Day 3
Day 4
Day 5
Day 6
Day 7
Day 8
*
Beacon A mean
Saline A mean

Fig.11C

Beacon v. Body Weight and % Fat in Group A animals

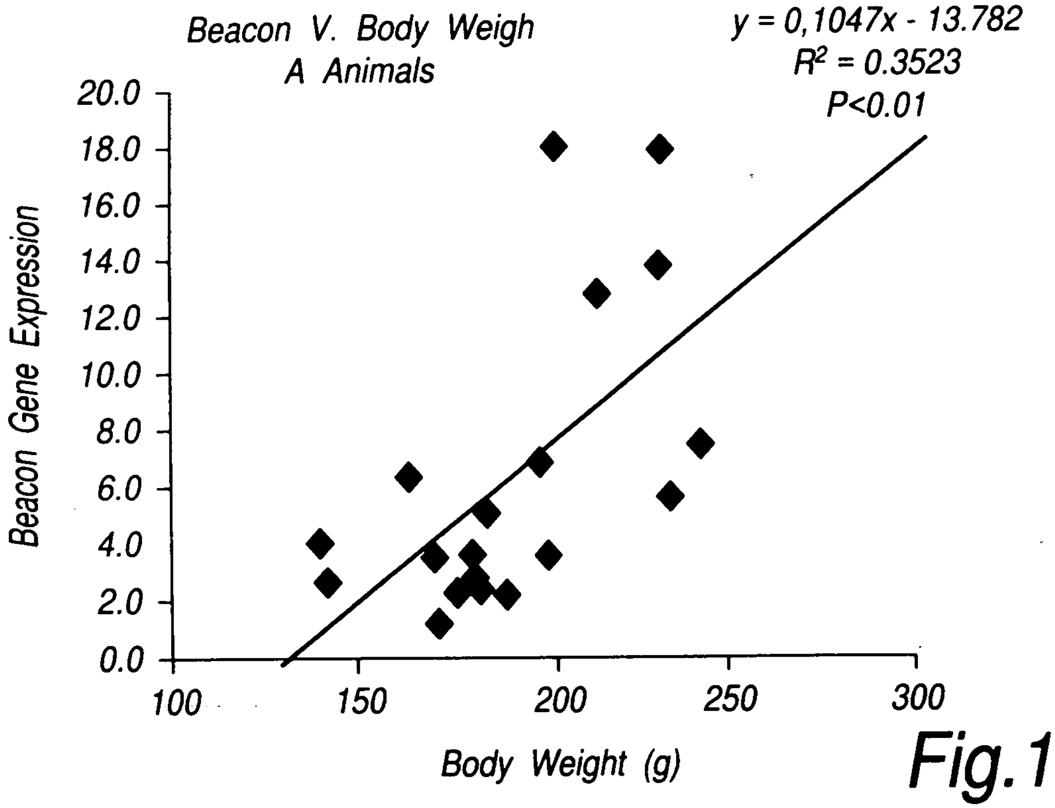


Fig.12A

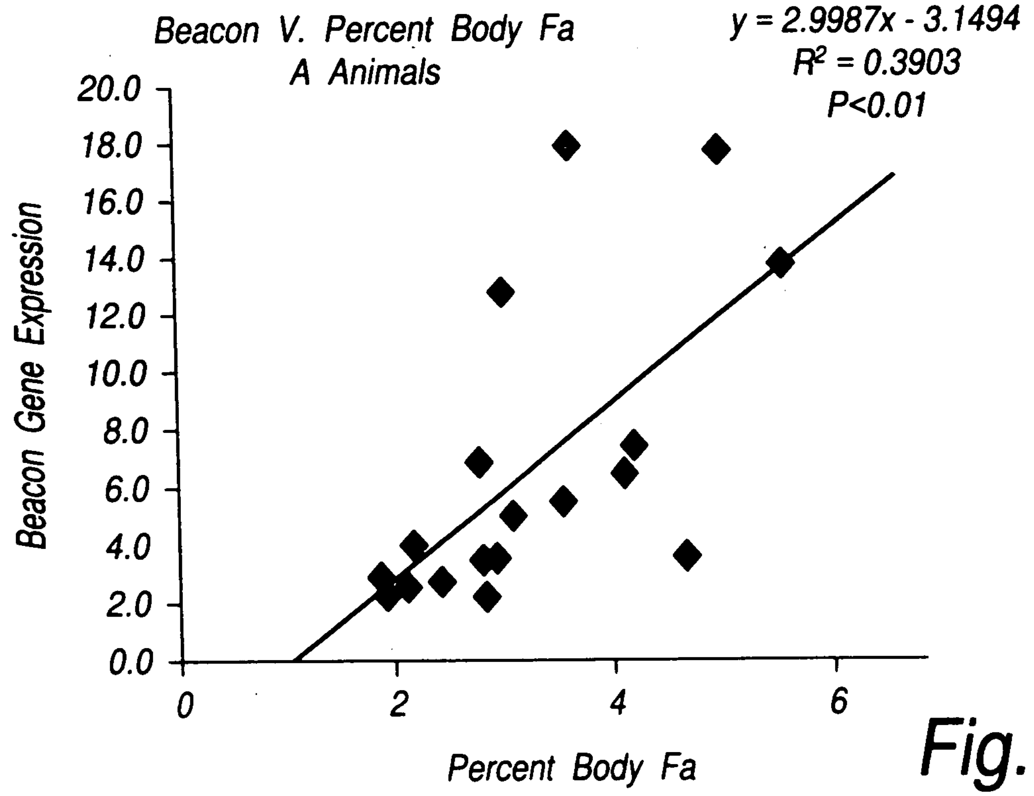


Fig.12B

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS 435 | SUBCLASS 69.1

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Beacon v. % Body Fat

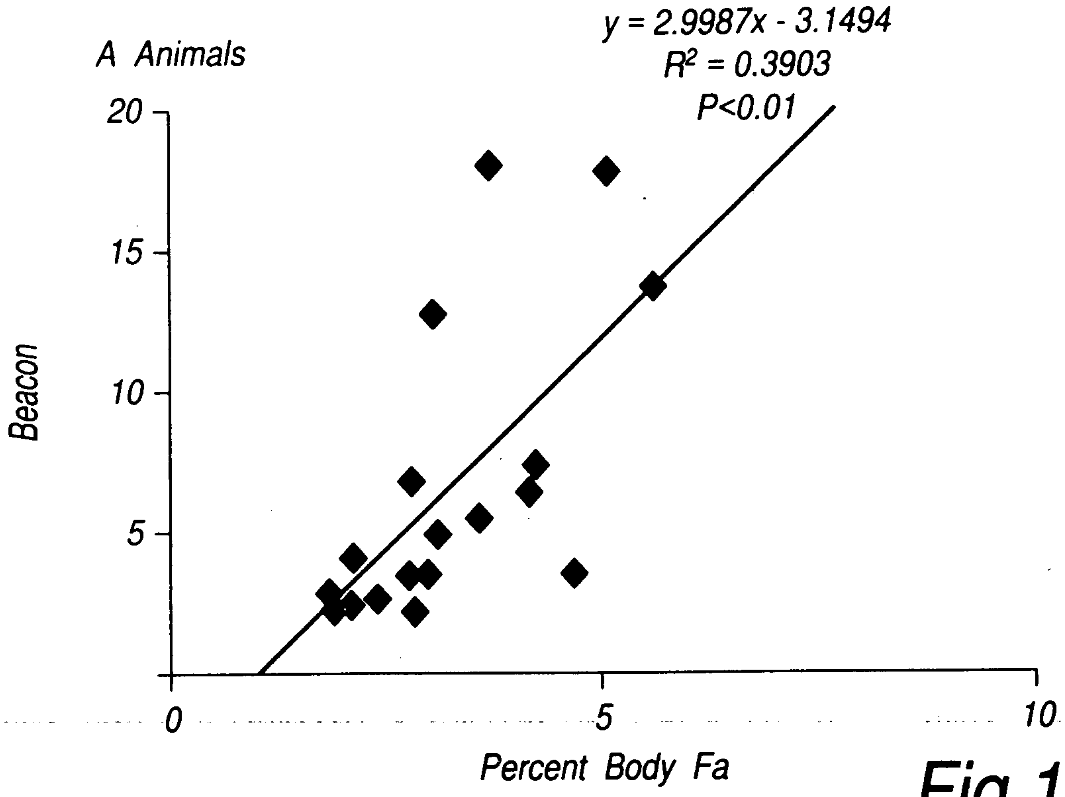

Fig.13A

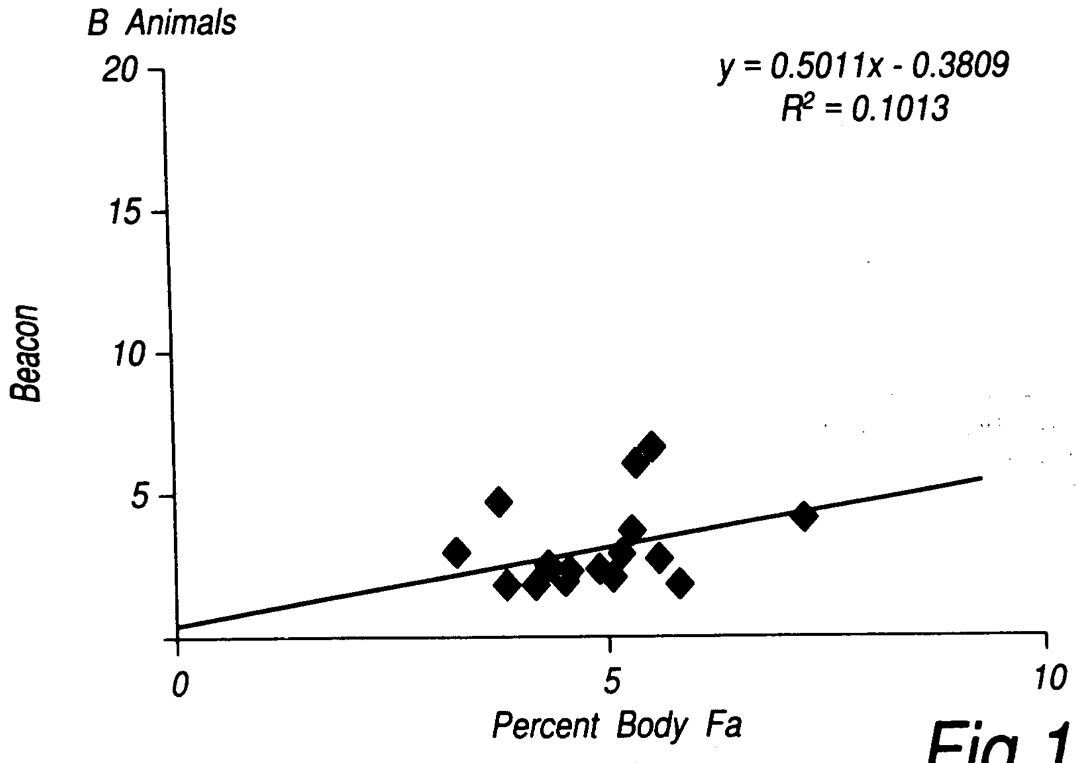

Fig.13B